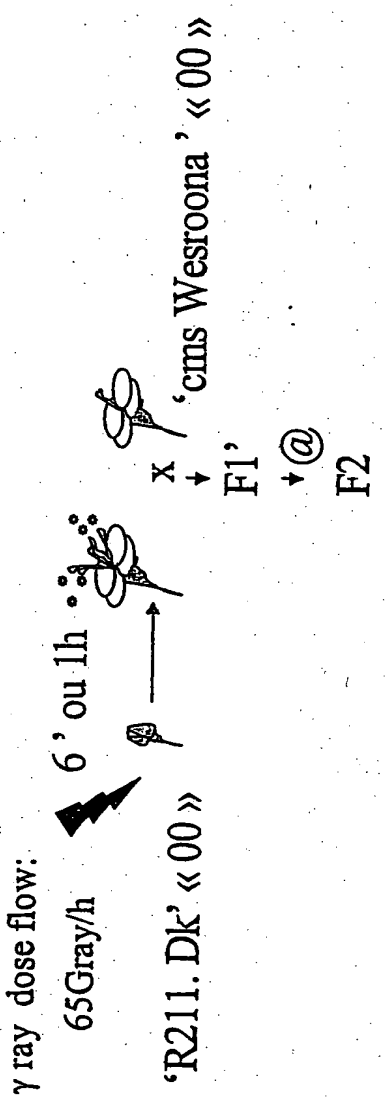
Fig 1



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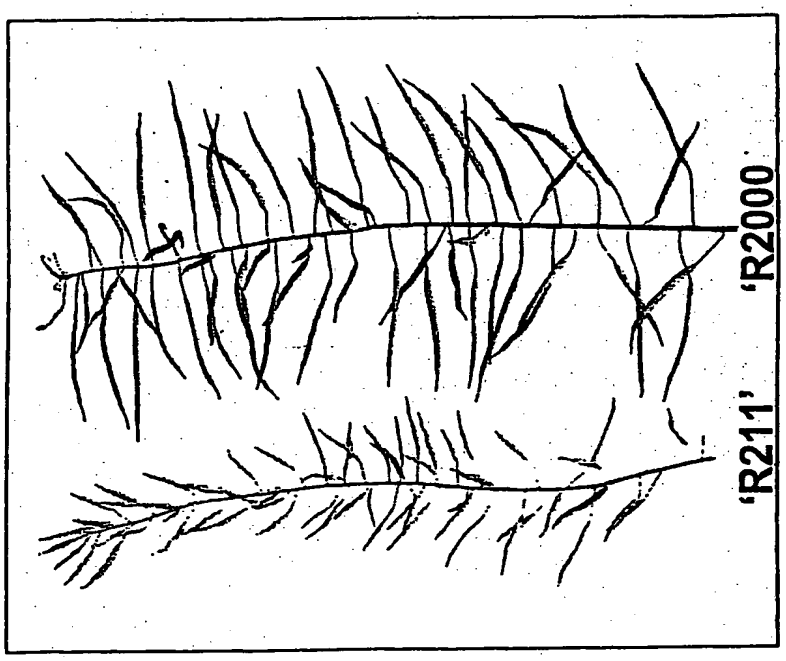


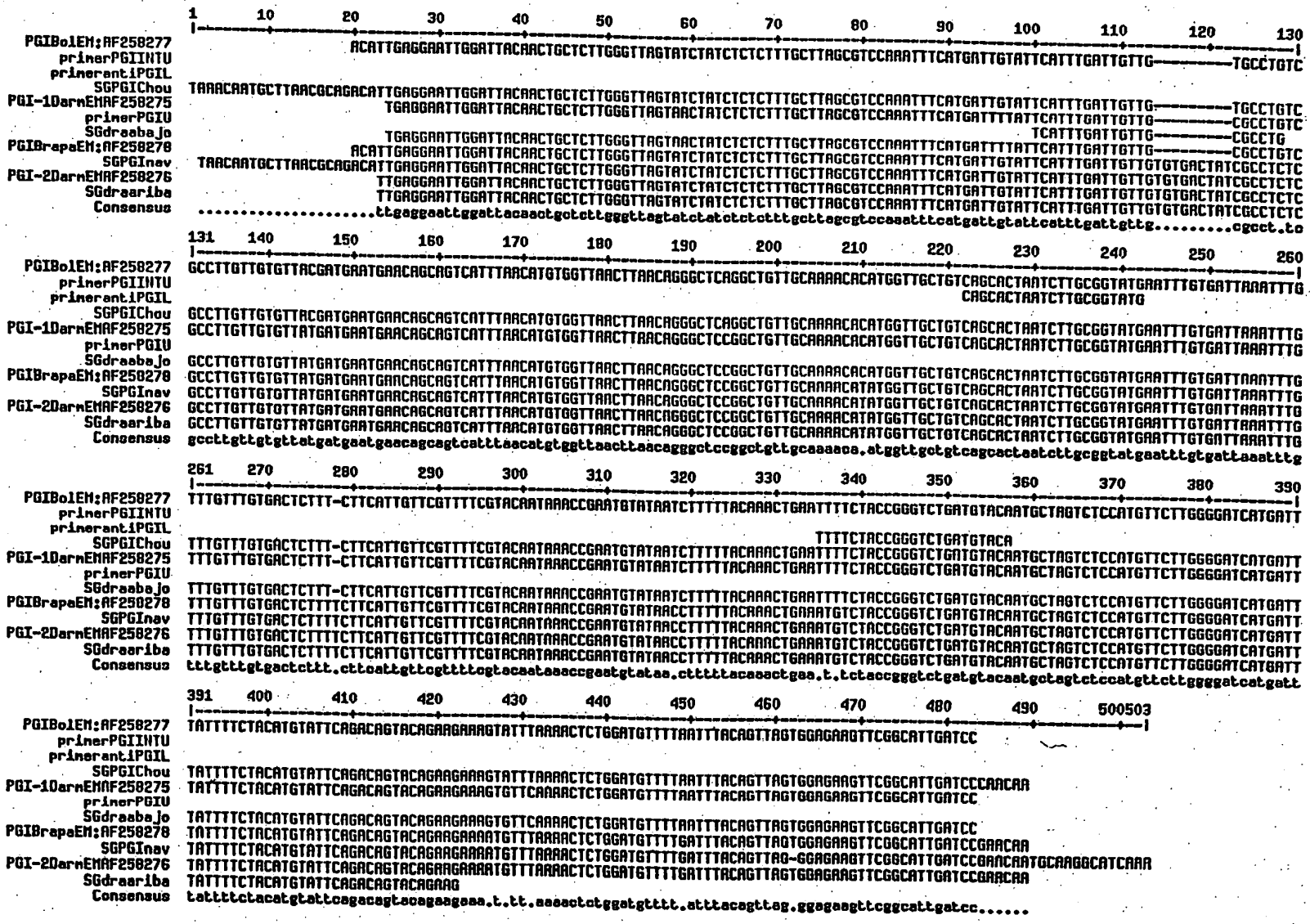
Fig. 1: Seed set on 'R211' and 'R2000'

Fig 2

Fig 3

Genotype	Selfings	Test Crosses
Drakkar	29.3	
Pactol	23.1	
R211	11.2	25.5
R2000	**26. 5** (24.0 – 31.1)	**27.0** (24.0 – 28.7)

Fig 4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Consensus

Fig 5

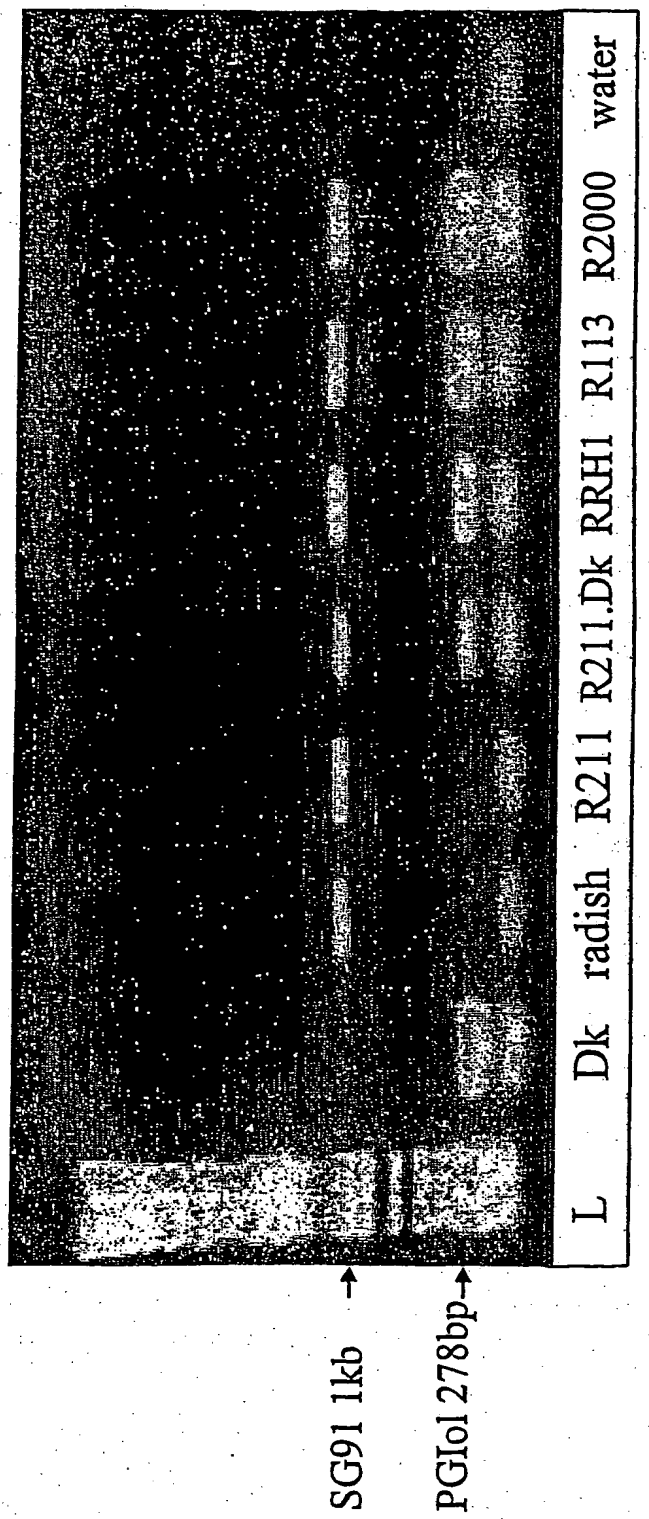
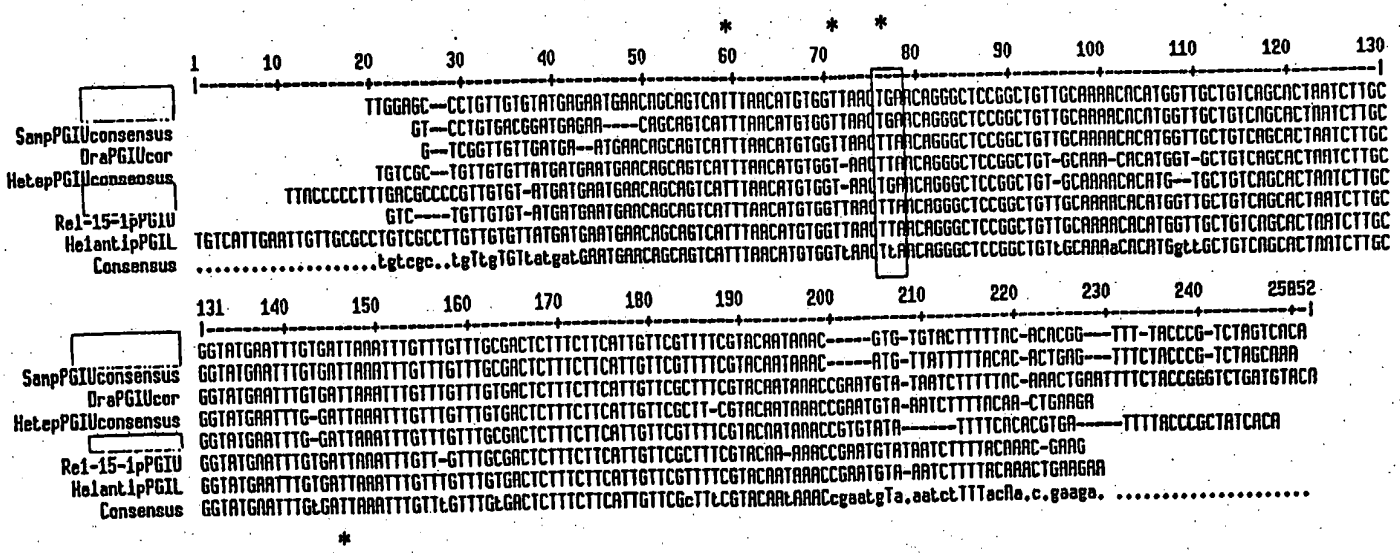
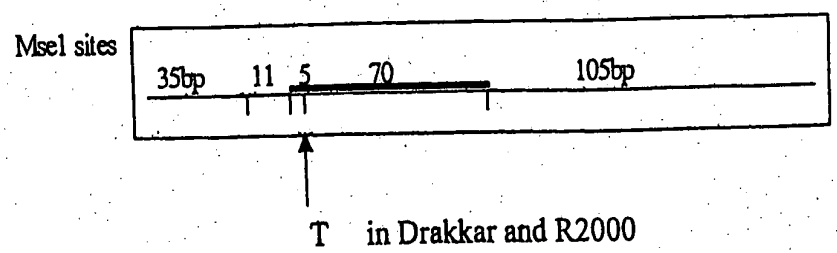

L
Dk
radish
R211
R211.Dk
RRH1
R113
R2000
water
SG91 1kb
PGIol 278bp

Fig 6





MseI restriction enzyme cut DNA sequences at the T/TAA sites (*)

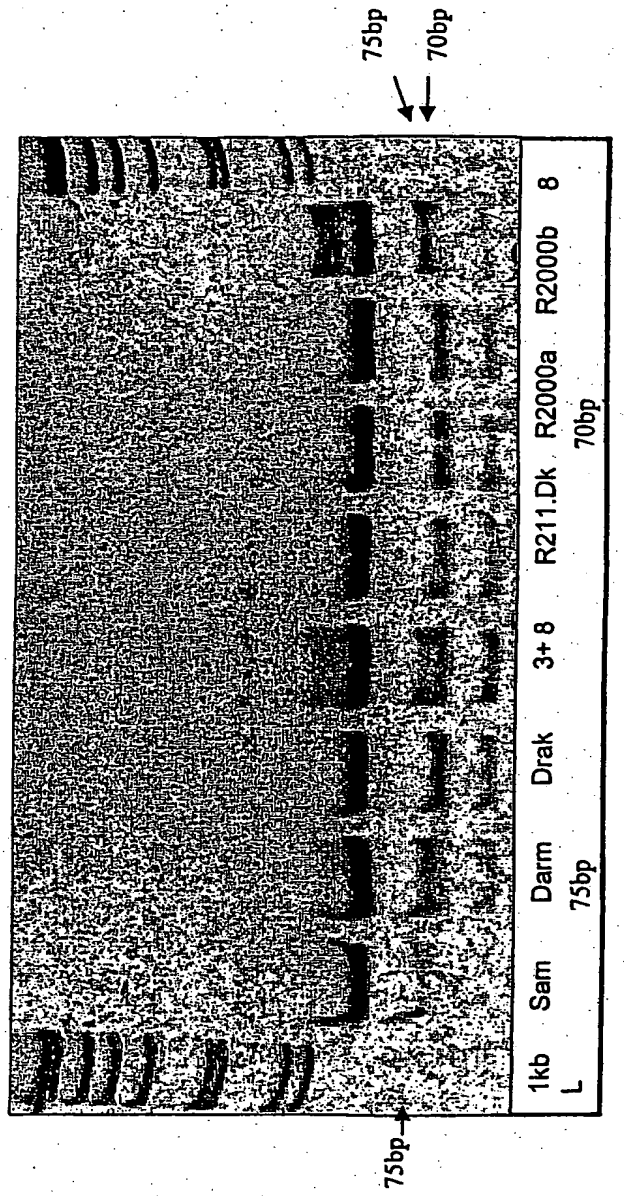
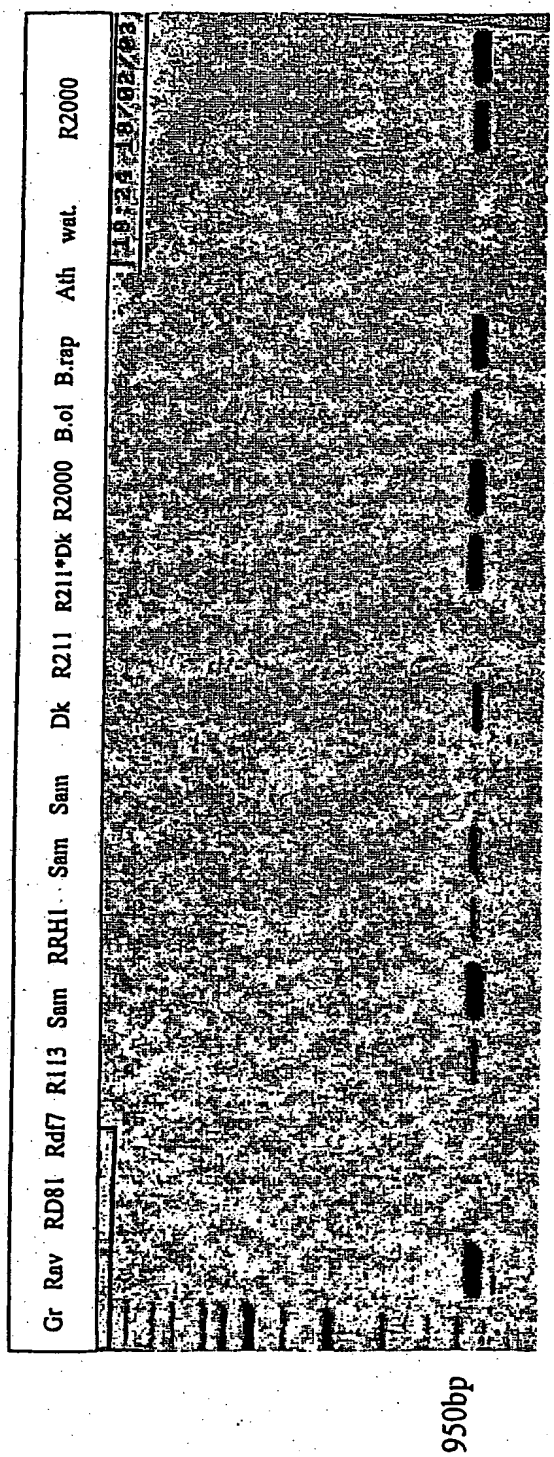

75bp
70bp
1kb L
Sam
Darm
75bp
Drak
3+8
R211.Dk
R2000a
70bp
R2000b
8
75bp

Fig 7

Fig 8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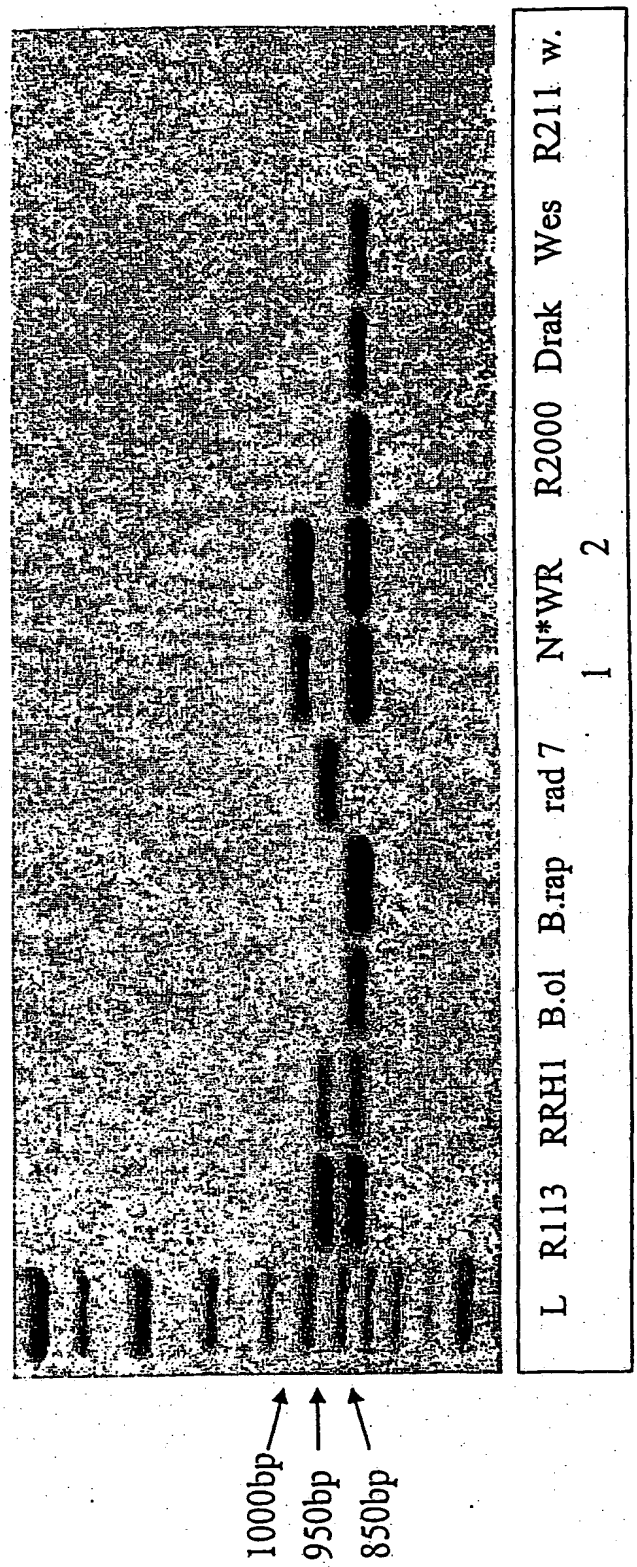
950bp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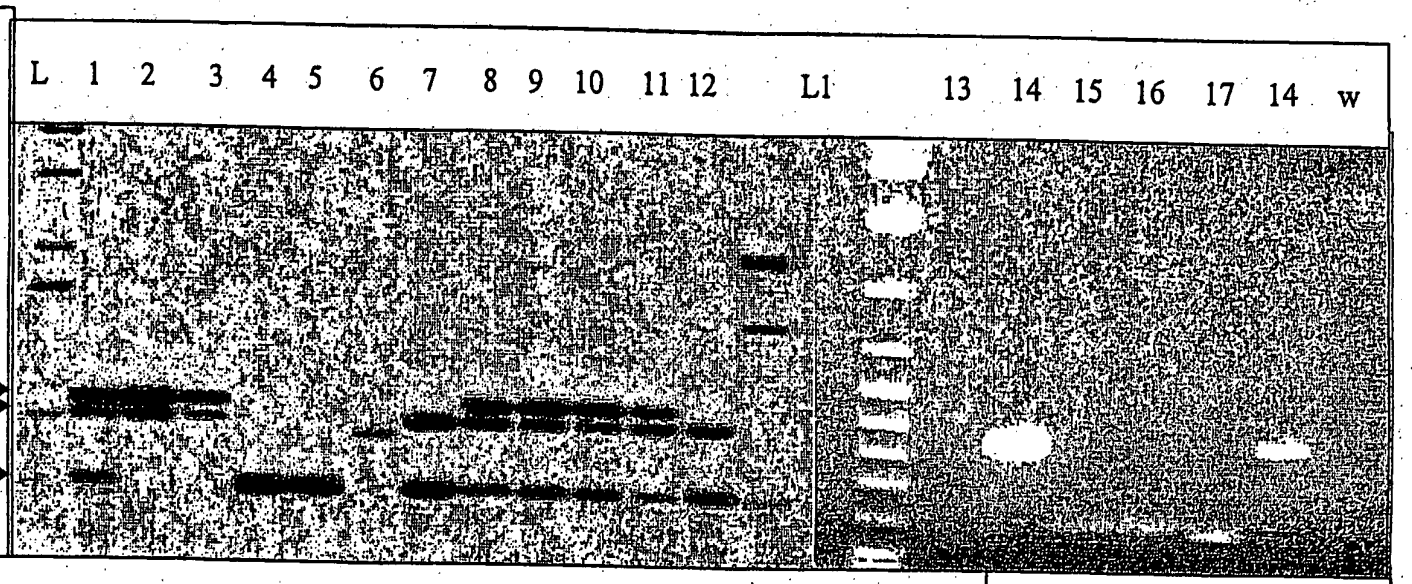
1000bp
950bp
850bp

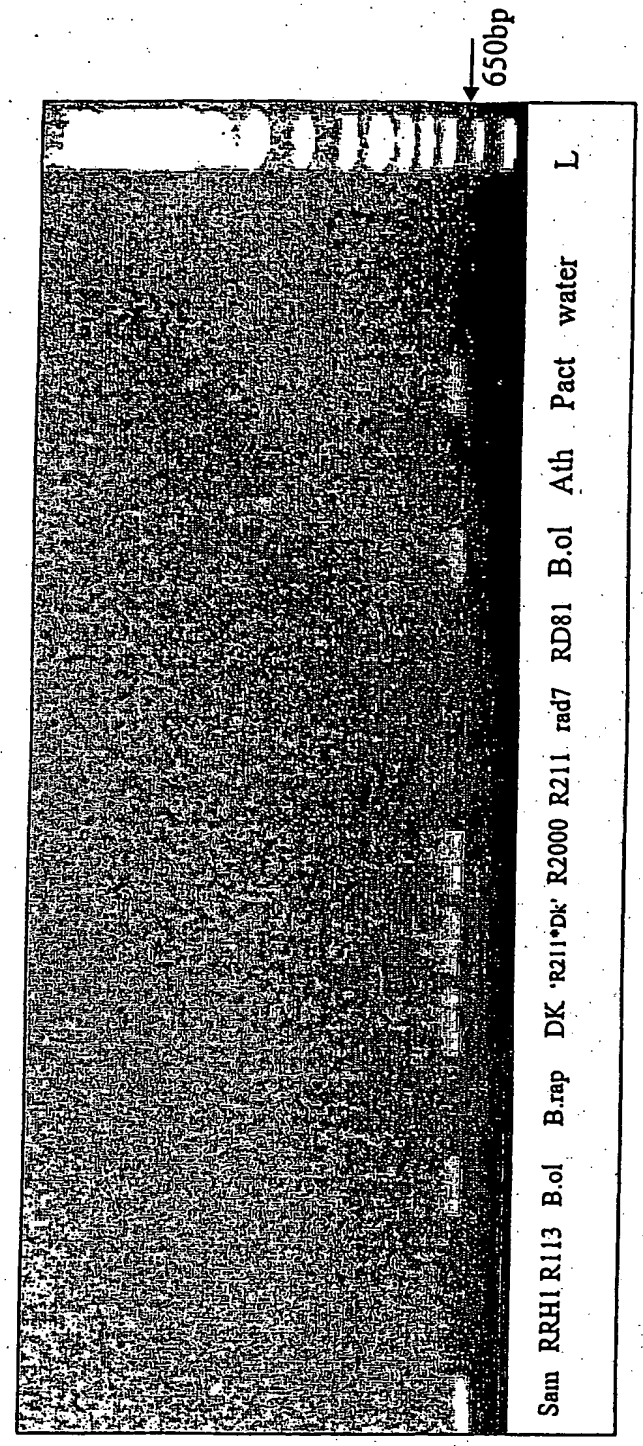
Fig 9

Fig 10



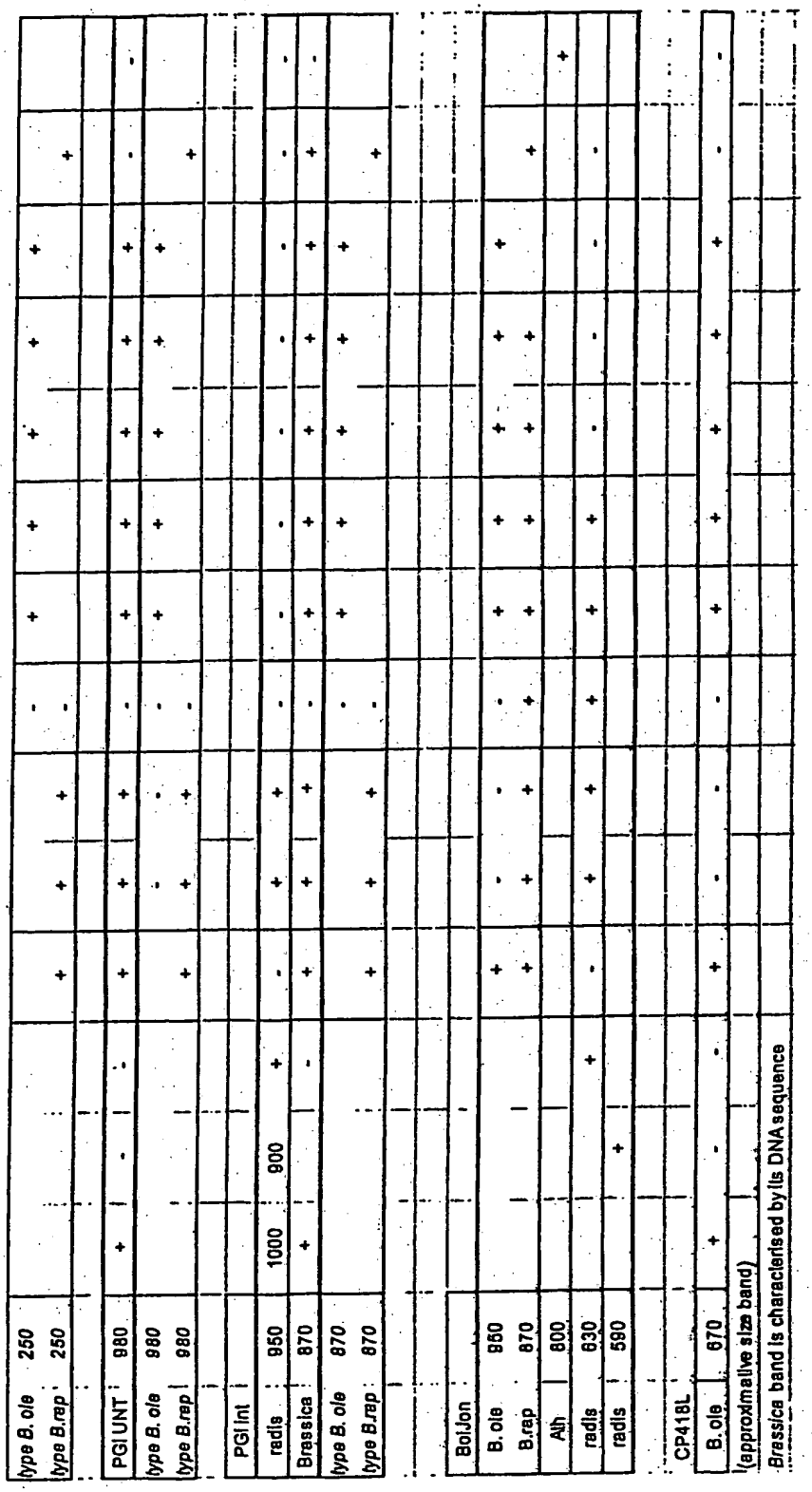
BolJon PCR bands (bp) n°		a	b	c	d	e
4,5	radish species:line 7				600	
17	radish RD81					590
14	B.rapa species		870			
13	B.oleracea species	950				
6	Arabidopsis thaliana (WS)			800		
2, 3	maintainer rapeseed: 2 Samourai; 3 Pactol	950	870			
7,12	homozygous restored rapeseed: 7 Samourai RRH1, 12 R211	0	870		600	
11	incomplete restored SRfi	950	870		600	
1,8	heterozygous restored rapeseed: R211.Dk	950	870		600	
9,10	homozygous restored R2000: 6 lineE38, 8,18,19 line R1.15	950	870		600	
L , L1	ladder1kb+, Ladder 100bp					

Fig 11



The CP418 band (about 650bp) specific to the B.oleracea genome.
It is present in B.ol, B.napus (Samourai, Drakkar, Pactol and the herterozygous R211*Dk)
It is absent from the restored rapeseed (RRH, R113 and R211)
It is present in the homozygous R2000.

Figure 12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type B.rap 250
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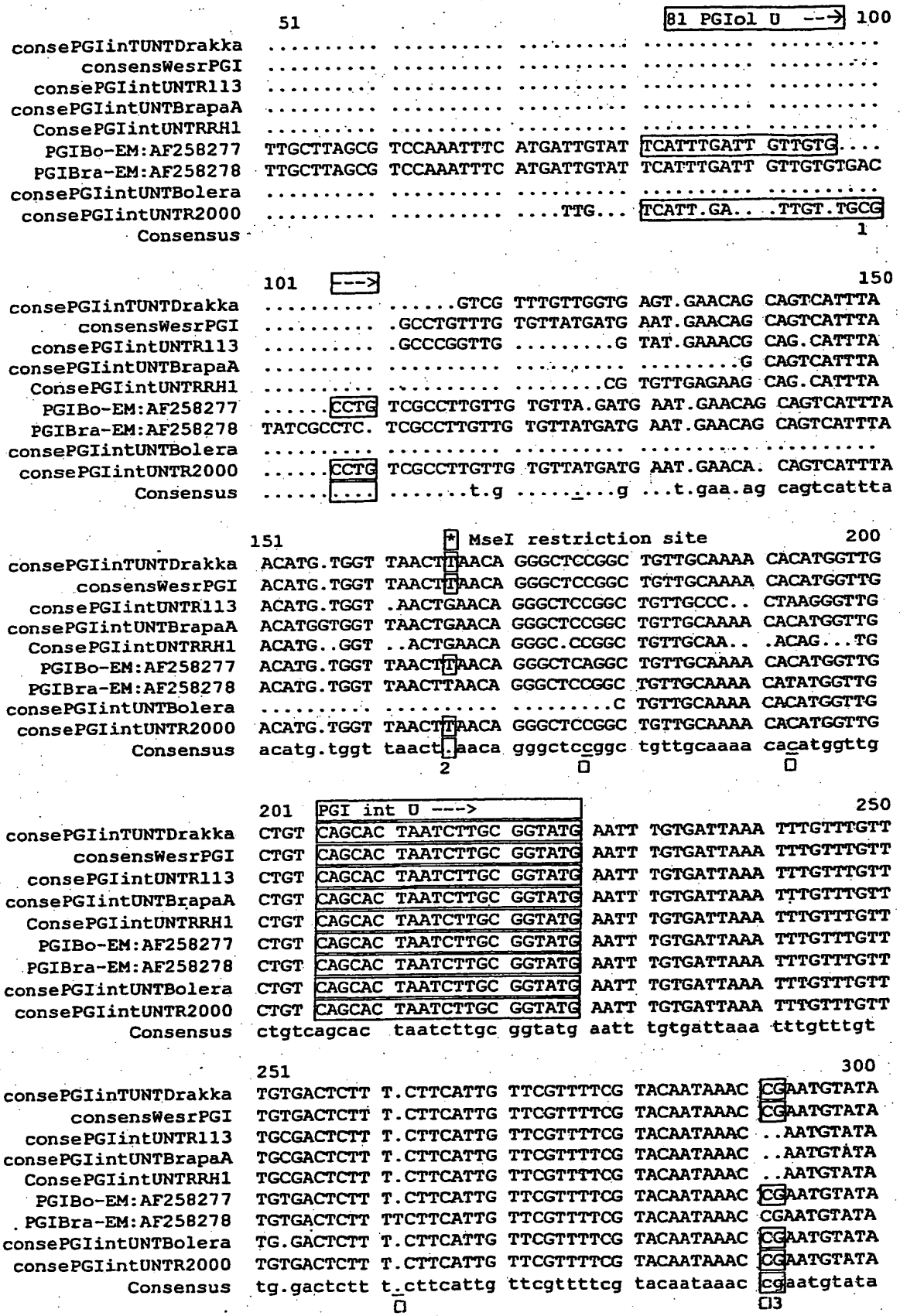
type B. ole 980
type B.rap 980
PGI Int
radis 950
Brassica 870
type B. ole 870
type B.rap 870
BolJon
B. ole 960
B.rap 870
Ath 800
radis 630
radis 590
CP418L
B. ole 670
(approximative size band)
Brassica band is characterised by its DNA sequence

Figure 13 (a)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Consensus
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151
* MseI restriction site
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201
PGI int U --->
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251
300

Figure 13 (b)

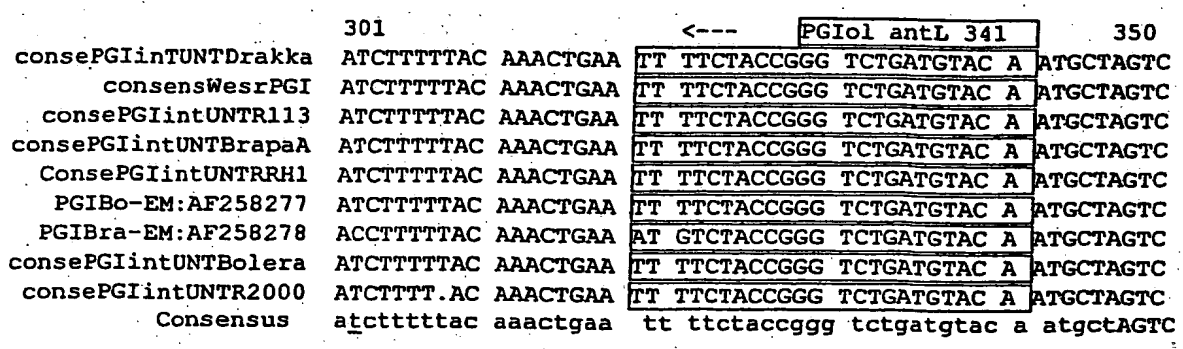
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Figure 14 (a)

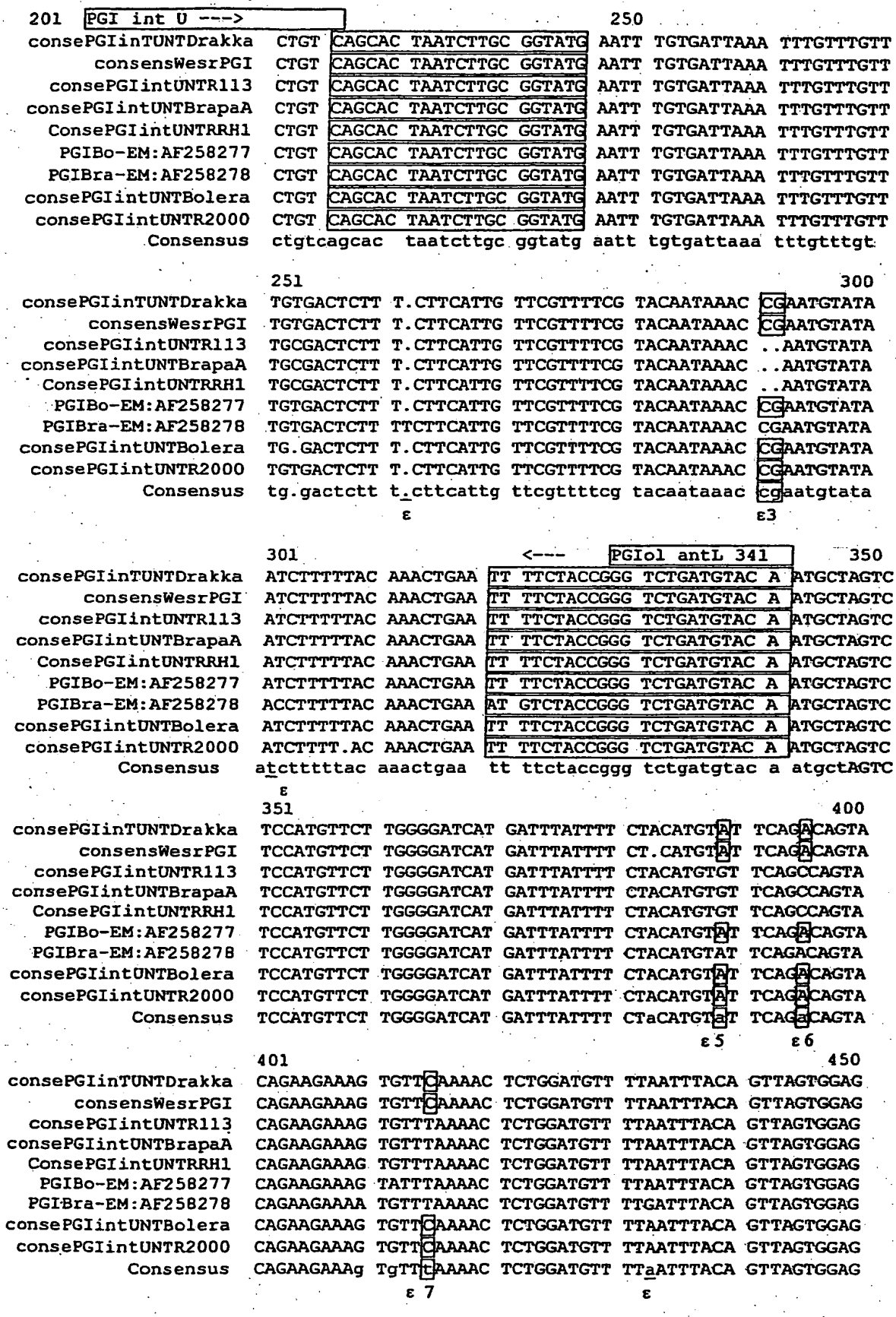
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Figure 14 (b)

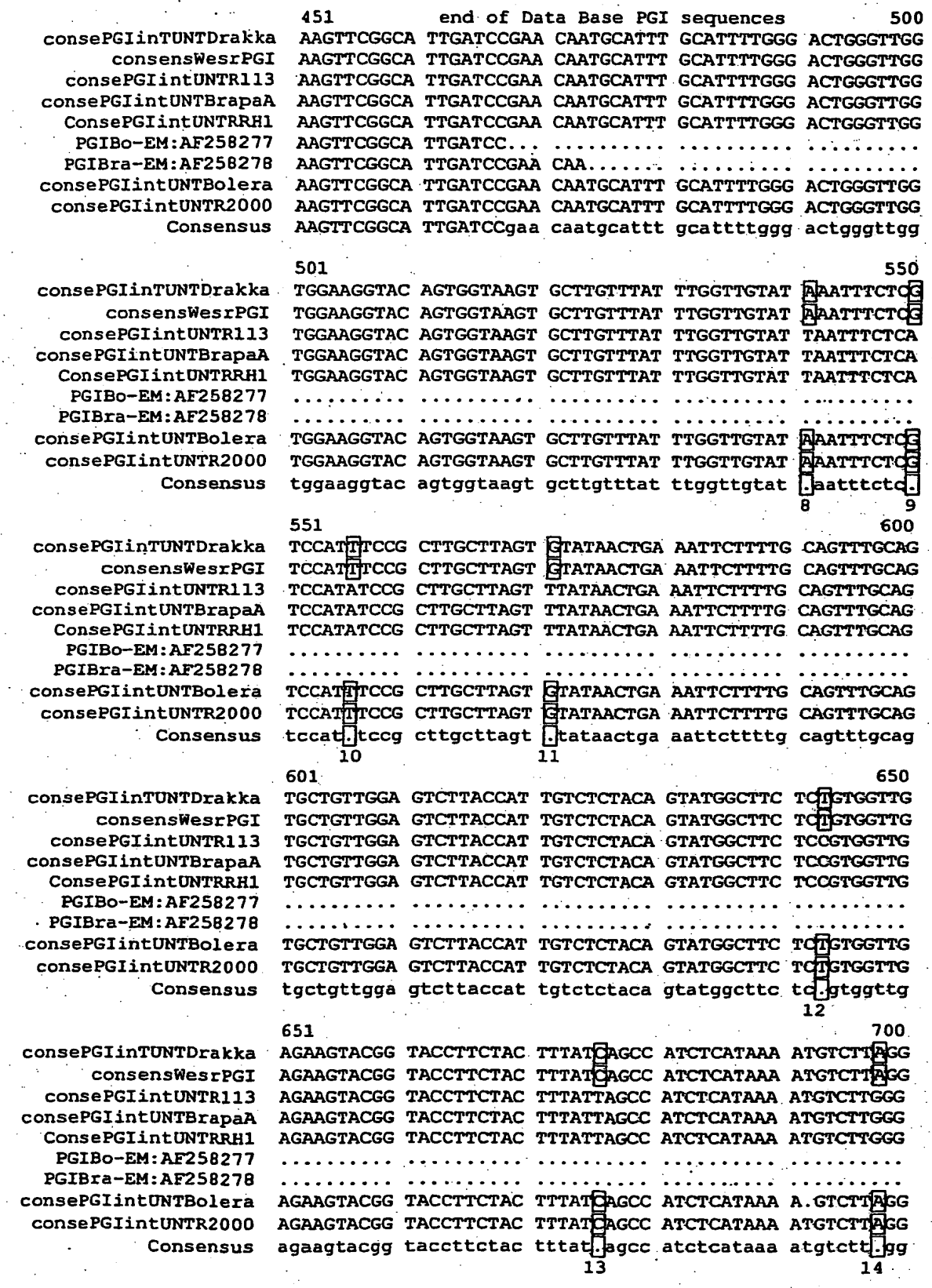
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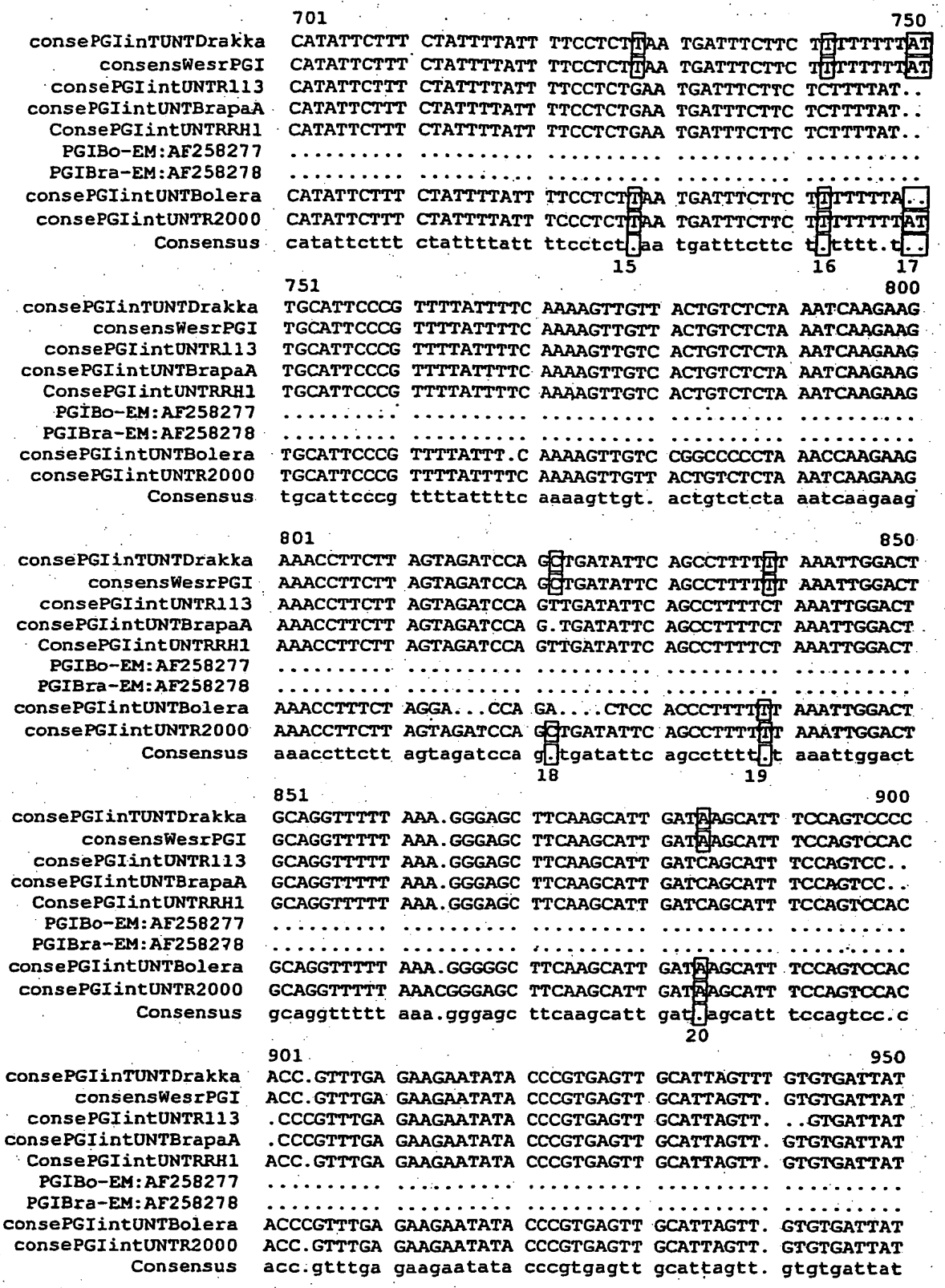
Figure 14 (c)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Consensus aaaccttctt agtagatcca g.tgatattc agcctttt.t aaattggact
18 19
851 900
consePGIintUNTDrakka GCAGGTTTTT AAA.GGGAGC TTCAAGCATT GATAAGCATT TCCAGTCCCC
consensWesrPGI GCAGGTTTTT AAA.GGGAGC TTCAAGCATT GATAAGCATT TCCAGTCCAC
consePGIintUNTR113 GCAGGTTTTT AAA.GGGAGC TTCAAGCATT GATCAGCATT TCCAGTCC..
consePGIintUNTBrapaA GCAGGTTTTT AAA.GGGAGC TTCAAGCATT GATCAGCATT TCCAGTCC..
ConsePGIintUNTRRH1 GCAGGTTTTT AAA.GGGAGC TTCAAGCATT GATCAGCATT TCCAGTCCAC
PGIBo-EM:AF258277 ....
PGIBra-EM:AF258278 ....
consePGIintUNTBolera GCAGGTTTTT AAA.GGGGGC TTCAAGCATT GATAAGCATT TCCAGTCCAC
consePGIintUNTR2000 GCAGGTTTTT AAACGGGAGC TTCAAGCATT GATAAGCATT TCCAGTCCAC
Consensus gcaggttttt aaa.gggagc ttcaagcatt gat.agcatt tccagtcc.c
20
901 950
consePGIintUNTDrakka ACC.GTTTGA GAAGAATATA CCCGTGAGTT GCATTAGTTT GTGTGATTAT
consensWesrPGI ACC.GTTTGA GAAGAATATA CCCGTGAGTT GCATTAGTT. GTGTGATTAT
consePGIintUNTR113 .CCCGTTTGA GAAGAATATA CCCGTGAGTT GCATTAGTT. ..GTGATTAT
consePGIintUNTBrapaA .CCCGTTTGA GAAGAATATA CCCGTGAGTT GCATTAGTT. GTGTGATTAT
ConsePGIintUNTRRH1 ACC.GTTTGA GAAGAATATA CCCGTGAGTT GCATTAGTT. GTGTGATTAT
PGIBo-EM:AF258277 ....
PGIBra-EM:AF258278 ....
consePGIintUNTBolera ACCCGTTTGA GAAGAATATA CCCGTGAGTT GCATTAGTT. GTGTGATTAT
consePGIintUNTR2000 ACC.GTTTGA GAAGAATATA CCCGTGAGTT GCATTAGTT. GTGTGATTAT
Consensus acc.gtttga gaagaatata cccgtgagtt gcattagtt. gtgtgattat

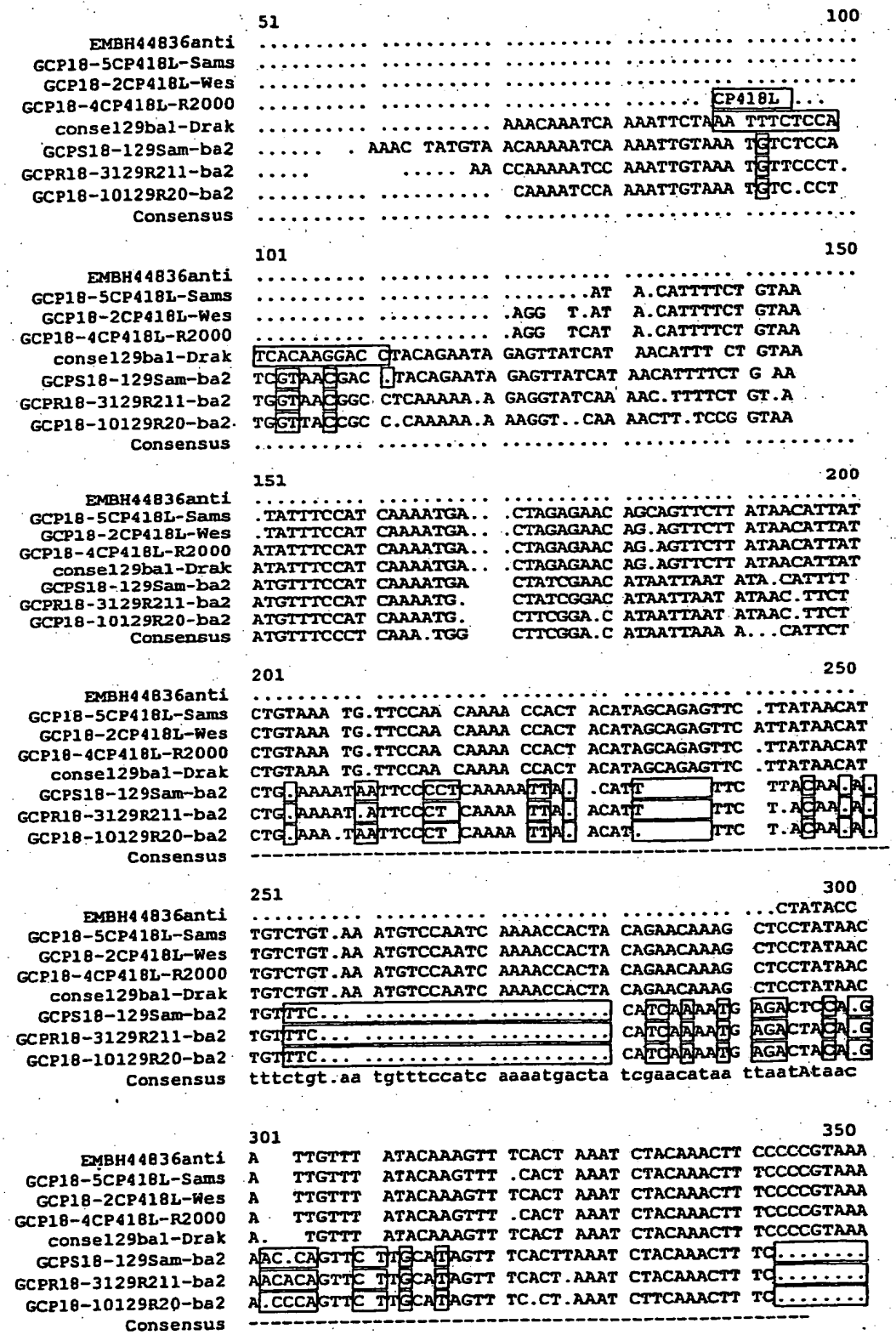
Figure 14 (d)

```
                          951                                                1000
consePGIinTUNTDrakka      ACAGTTTTTC TTGTCTTTTT GCTATGCCCA TCAACACTAG AAGATTCGTG
     consensWesrPGI       ACAGTTTT.C TTGTCTTTT. GCTATGTCCA TCAACACTAG A.GATTCGTG
  consePGIintUNTR113      ACAGTTTT.C TTGCCTTTTT GCTAT..AGG GCAAC.CTAG A.GATTCATG
consePGIintUNTBrapaA      ACAGTTTT.C TTGTCTTTT. GCTATG.TCA TCAAC.CTAG A.GATTCATG
  ConsePGIintUNTRRH1      ACAGTTTT.C TTGTCTTTTT GCTAT...AT GCAACCCTAG ..GATTCATG
   PGIBo-EM:AF258277      .......... .......... .......... .......... ..........
   PGIBra-EM:AF258278     .......... .......... .......... .......... ..........
consePGIintUNTBolera      ACAGTTTT.C TTGTCTTTTT GCTAG..TGA TCAAC.CTAG A.GATTCGTG
 consePGIintUNTR2000      ACAGTTTT.C TTGTCTTTTT GCTATGTCCA TCAACACTAG A.GATTCGTG
           Consensus      acagtttt.c ttgtcttttt gctat....a tcaac.ctag a.gattc.tg
                                                                          21

                          1001                                               1050
consePGIinTUNTDrakka      AAGTTATTAG TGTAGCCAAC GCCTAGGGGG AGGTTGGTTG GCTGTTTTGG
     consensWesrPGI       AAGTTATTAG TGTAGTCAAC GCA....... .......... ..........
  consePGIintUNTR113      AAGTTATTAG TGTAGTCAAC GCAGAGGAGA G..TTCACTG ACGG......
consePGIintUNTBrapaA      AAGTTATTAG TGTAGTCAAC GCAGAGTGAG AGG.TGATTG ..........
  ConsePGIintUNTRRH1      AAGTTATTAG TGTAGTCAAC GCAGAGGAGG AGATGGTT.. ..........
   PGIBo-EM:AF258277      .......... .......... .......... .......... ..........
   PGIBra-EM:AF258278     .......... .......... .......... .......... ..........
consePGIintUNTBolera      AAGTTATTAG TGTAGTCAAC GCATAGGAGG AGC....... ..........
 consePGIintUNTR2000      AAGTTATTAG TGTAGTCAAC GCATAGGGAG AGGTGAT.GG TGACTTTTGG
           Consensus      aagttattag tgtagtcaac gca.agg.g. .g........ ..........

                          1051                    1076
consePGIinTUNTDrakka      ACGTTTTCAC GTGCTCCGGG GGGTTTTTGG GGACCAAACC CCCAAC
     consensWesrPGI       .......... .......... .......... .......... ......
  consePGIintUNTR113      .......... .......... .......... .......... ......
consePGIintUNTBrapaA      .......... .......... .......... .......... ......
  ConsePGIintUNTRRH1      .......... .......... .......... .......... ......
   PGIBo-EM:AF258277      .......... .......... .......... .......... ......
   PGIBra-EM:AF258278     .......... .......... .......... .......... ......
consePGIintUNTBolera      .......... .......... .......... .......... ......
 consePGIintUNTR2000      ACGATTTCAG GTGCTTTAGG GTTATTG..... .......... ..........
```

Figure 15 (a)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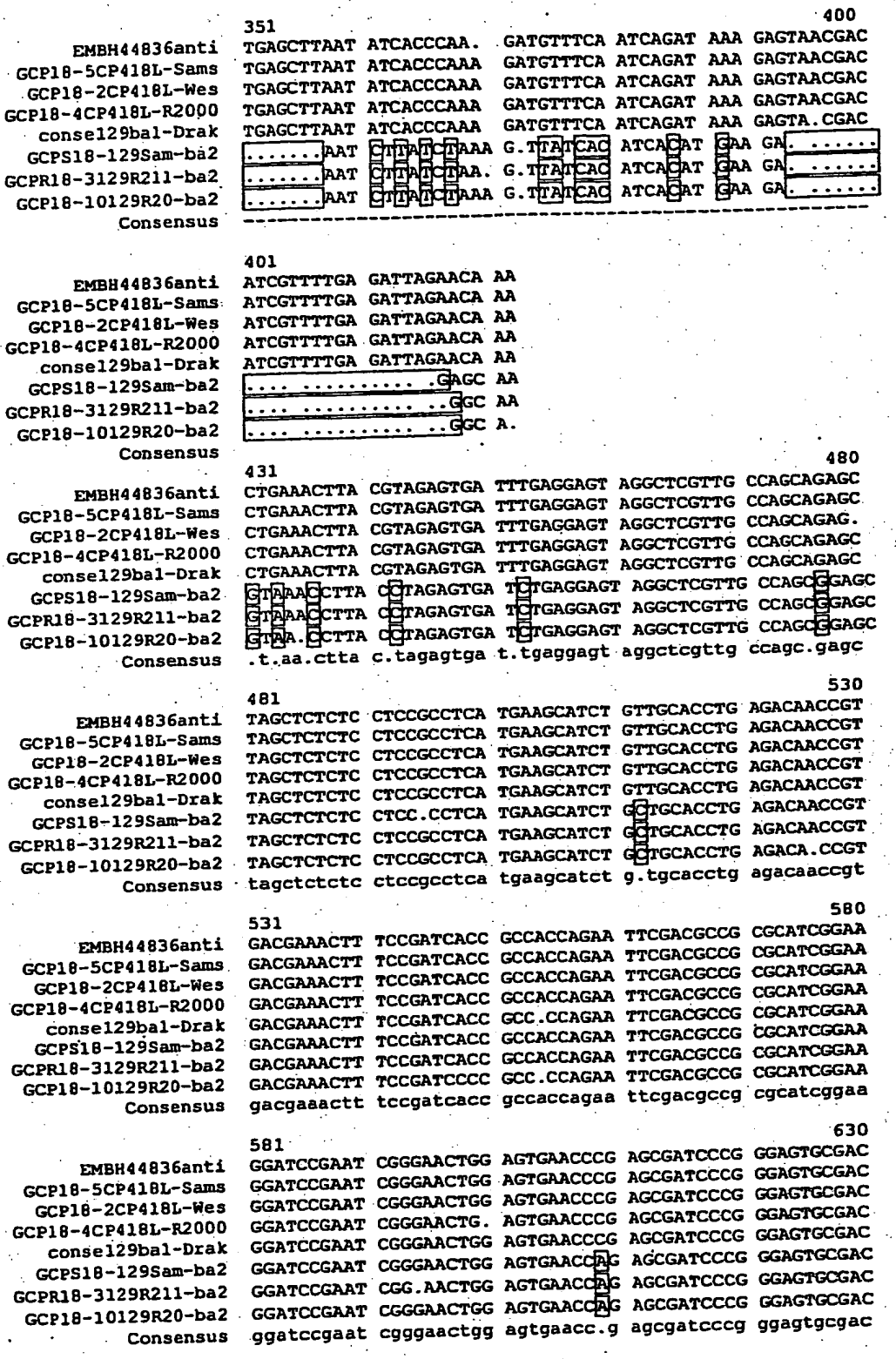
GCP18-5CP418L-Sams
GCP18-2CP418L-Wes
GCP18-4CP418L-R2000
CP418L
conse129bal-Drak
GCPS18-129Sam-ba2
GCPR18-3129R211-ba2
GCP18-10129R20-ba2
Consensus
101
150
151
200
201
250
251
300
301
350

Figure 15 (b)


351 400
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GCP18-5CP418L-Sams TGAGCTTAAT ATCACCCAAA GATGTTTCA ATCAGAT AAA GAGTAACGAC
GCP18-2CP418L-Wes TGAGCTTAAT ATCACCCAAA GATGTTTCA ATCAGAT AAA GAGTAACGAC
GCP18-4CP418L-R2000 TGAGCTTAAT ATCACCCAAA GATGTTTCA ATCAGAT AAA GAGTAACGAC
conse129bal-Drak TGAGCTTAAT ATCACCCAAA GATGTTTCA ATCAGAT AAA GAGTA.CGAC
GCPS18-129Sam-ba2 .....AAT CTTAATCTAAA G.TTATCAC ATCACAT GAA GA. .....
GCPR18-3129R211-ba2 .....AAT CTTAATCTAA. G.TTATCAC ATCACAT GAA GA. .....
GCP18-10129R20-ba2 .....AAT CTTAATCTAAA G.TTATCAC ATCACAT GAA GA. .....
Consensus
401
EMBH44836anti ATCGTTTTGA GATTAGAACA AA
GCP18-5CP418L-Sams ATCGTTTTGA GATTAGAACA AA
GCP18-2CP418L-Wes ATCGTTTTGA GATTAGAACA AA
GCP18-4CP418L-R2000 ATCGTTTTGA GATTAGAACA AA
conse129bal-Drak ATCGTTTTGA GATTAGAACA AA
GCPS18-129Sam-ba2 .... .GAGC AA
GCPR18-3129R211-ba2 ....GGC AA
GCP18-10129R20-ba2 ....GGC A.
Consensus
431 480
EMBH44836anti CTGAAACTTA CGTAGAGTGA TTTGAGGAGT AGGCTCGTTG CCAGCAGAGC
GCP18-5CP418L-Sams CTGAAACTTA CGTAGAGTGA TTTGAGGAGT AGGCTCGTTG CCAGCAGAGC
GCP18-2CP418L-Wes CTGAAACTTA CGTAGAGTGA TTTGAGGAGT AGGCTCGTTG CCAGCAGAG.
GCP18-4CP418L-R2000 CTGAAACTTA CGTAGAGTGA TTTGAGGAGT AGGCTCGTTG CCAGCAGAGC
conse129bal-Drak CTGAAACTTA CGTAGAGTGA TTTGAGGAGT AGGCTCGTTG CCAGCAGAGC
GCPS18-129Sam-ba2 GTAAACCTTA CGTAGAGTGA TCTGAGGAGT AGGCTCGTTG CCAGCGGAGC
GCPR18-3129R211-ba2 GTAAACCTTA CGTAGAGTGA TCTGAGGAGT AGGCTCGTTG CCAGCGGAGC
GCP18-10129R20-ba2 GTAA.CCTTA CGTAGAGTGA TCTGAGGAGT AGGCTCGTTG CCAGCGGAGC
Consensus .t.aa.ctta c.tagagtga t.tgaggagt aggctcgttg ccagc.gagc
481 530
EMBH44836anti TAGCTCTCTC CTCCGCCTCA TGAAGCATCT GTTGCACCTG AGACAACCGT
GCP18-5CP418L-Sams TAGCTCTCTC CTCCGCCTCA TGAAGCATCT GTTGCACCTG AGACAACCGT
GCP18-2CP418L-Wes TAGCTCTCTC CTCCGCCTCA TGAAGCATCT GTTGCACCTG AGACAACCGT
GCP18-4CP418L-R2000 TAGCTCTCTC CTCCGCCTCA TGAAGCATCT GTTGCACCTG AGACAACCGT
conse129bal-Drak TAGCTCTCTC CTCCGCCTCA TGAAGCATCT GTTGCACCTG AGACAACCGT
GCPS18-129Sam-ba2 TAGCTCTCTC CTCC.CCTCA TGAAGCATCT GCTGCACCTG AGACAACCGT
GCPR18-3129R211-ba2 TAGCTCTCTC CTCCGCCTCA TGAAGCATCT GCTGCACCTG AGACAACCGT
GCP18-10129R20-ba2 TAGCTCTCTC CTCCGCCTCA TGAAGCATCT GCTGCACCTG AGACA.CCGT
Consensus tagctctctc ctccgcctca tgaagcatct g.tgcacctg agacaaccgt
531 580
EMBH44836anti GACGAAACTT TCCGATCACC GCCACCAGAA TTCGACGCCG CGCATCGGAA
GCP18-5CP418L-Sams GACGAAACTT TCCGATCACC GCCACCAGAA TTCGACGCCG CGCATCGGAA
GCP18-2CP418L-Wes GACGAAACTT TCCGATCACC GCCACCAGAA TTCGACGCCG CGCATCGGAA
GCP18-4CP418L-R2000 GACGAAACTT TCCGATCACC GCC.CCAGAA TTCGACGCCG CGCATCGGAA
conse129bal-Drak GACGAAACTT TCCGATCACC GCCACCAGAA TTCGACGCCG CGCATCGGAA
GCPS18-129Sam-ba2 GACGAAACTT TCCGATCACC GCCACCAGAA TTCGACGCCG CGCATCGGAA
GCPR18-3129R211-ba2 GACGAAACTT TCCGATCACC GCCACCAGAA TTCGACGCCG CGCATCGGAA
GCP18-10129R20-ba2 GACGAAACTT TCCGATCCCC GCC.CCAGAA TTCGACGCCG CGCATCGGAA
Consensus gacgaaactt tccgatcacc gccaccagaa ttcgacgccg cgcatcggaa
581 630
EMBH44836anti GGATCCGAAT CGGGAACTGG AGTGAACCCG AGCGATCCCG GGAGTGCGAC
GCP18-5CP418L-Sams GGATCCGAAT CGGGAACTGG AGTGAACCCG AGCGATCCCG GGAGTGCGAC
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GCP18-4CP418L-R2000 GGATCCGAAT CGGGAACTG. AGTGAACCCG AGCGATCCCG GGAGTGCGAC
conse129bal-Drak GGATCCGAAT CGGGAACTGG AGTGAACCCG AGCGATCCCG GGAGTGCGAC
GCPS18-129Sam-ba2 GGATCCGAAT CGGGAACTGG AGTGAACCAG AGCGATCCCG GGAGTGCGAC
GCPR18-3129R211-ba2 GGATCCGAAT CGG.AACTGG AGTGAACCAG AGCGATCCCG GGAGTGCGAC
GCP18-10129R20-ba2 GGATCCGAAT CGGGAACTGG AGTGAACCAG AGCGATCCCG GGAGTGCGAC
Consensus ggatccgaat cgggaactgg agtgaacc.g agcgatcccg ggagtgcgac

Figure 15 (c)

```
                    631                                                690
          EMBH44836anti GGAGCGATGG GAAAAGAGAG TGGCACGATT TCGACGAAGA GTGGAAGAGG
        GCP18-5CP418L-Sams GGAGCGATGG GAAAAGAGAG TGGCACGATT TCGACGAAGA GTGGAAGAGG
         GCP18-2CP418L-Wes GGAGCGATGG GAAAAGAGAG TGGCACGATT TCGACGAAGA GTGGAAGAGG
      GCP18-4CP418L-R2000 GGAGCGATGG GAAAAGAGAG TGGCACGATT TCGACGAAGA GTGGAAGAGG
        consel29bal-Drak GGAGCGATGG GAAAAGAGAG TGGCACGATT TCGACGAA.A GTGGAAGAGG
       GCPS18-129Sam-ba2 GGAGCGTTGG AAAAAGAGAG TGGCACGATT TCGACGAAGA GAGGAAGAGG
      GCPR18-3129R211-ba2 GGAGCGTTGG AAAAAGAGAG TGGCACGATT TCGACGAAGA GAGGAAGAGG
       GCP18-10129R20-ba2 GGAGCGTTGG AAAAAGAGAG TGGCACGATT TCG.CGAAGA GAGGAAGAGG
                Consensus ggagcg.tgg .aaaagagag tggcacgatt tcgacgaaga g.ggaagagg

                    691                                                740
          EMBH44836anti AGAGGGTGGT GGATAAACTC GCGTATGATC AAGTTCGTCA TCGTCCTGAT
        GCP18-5CP418L-Sams AGAGGGTGGT GGATAAACTC GCGTATGATC AAGTTCGTCA TCGTCCTGAT
         GCP18-2CP418L-Wes AGAGGGTGGT GGATAAACTC GCGTATGATC AAGTTCGTCA TCGTCCTGAT
      GCP18-4CP418L-R2000 AGAGGGTGGT GGATAAACTC GCGTATGATC AAGTTCGTCA TCGTCCTGAT
        consel29bal-Drak AGAGGGTGGT GGATAAACTC GCGTATGATC AAGTTCGTCA TCGTCCTGAT
       GCPS18-129Sam-ba2 AGAGGGTGGT GGATAAACTC GCGTATGATC AAGTTCGTCA TCGTCCTGAT
      GCPR18-3129R211-ba2 AGAGG.TGGT GGATAAACTC GCGTATGATC AAGTTCGTCA TCGTCCTGAA
       GCP18-10129R20-ba2 AGAGGGTGGT GGATAAACTC GCGTATGATC AAGTTCGTCA TCGTCCTGAA
                Consensus agagggtggt ggataaactc gcgtatgatc aagttcgtca tcgtcctga.

                    741                                          pSG129antiU  790        800
          EMBH44836anti TGCCGCCATT TTTTTTGTCA GGGCGCTCTG TGGCTTAGAA GTTTCCGATG
        GCP18-5CP418L-Sams TGCCGCCATT TTTTTTGTCA GGGCGCTCTG TGGCTTAGAA GTTTCCGATG
         GCP18-2CP418L-Wes TGCCGCCATT TTTTTTGTCA GGGCGCTCTG TGGCTTAGAA GTTTCCGATG
      GCP18-4CP418L-R2000 TGCCGCCATT TTTTTTGTCA GGGCGCTCTG TGGCTTAGAA GTTTCCGTG.
        consel29bal-Drak TGCCGCCATT TTTTTTGTCA GGGCGCTCTG .GGCTTAGAA GTTTCCGA..
       GCPS18-129Sam-ba2 TGCCGCCATT CTTGTTCAC. .GGCGCTCTG GGT..... ..........
      GCPR18-3129R211-ba2 TGCCGCC... .......... .......... .......... ..........
       GCP18-10129R20-ba2 TGCC..CAT. CTTGAGCTC. .GG.GCGCGG GCTCACAA.. ..........
                Consensus tgccgccat. .tt.....c. .gg.gc.c.g ..........  ..........

                    791
          EMBH44836anti TCAATGAAC A GTGACACGAC GAAATGC
        GCP18-5CP418L-Sams TCAATGAAAC AGAAT...TC CGGG...
         GCP18-2CP418L-Wes CCAATGAACA AGATTATTTC CGATG..
      GCP18-4CP418L-R2000 .......... .......... .......
        consel29bal-Drak .......... .......... .......
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Figure 16

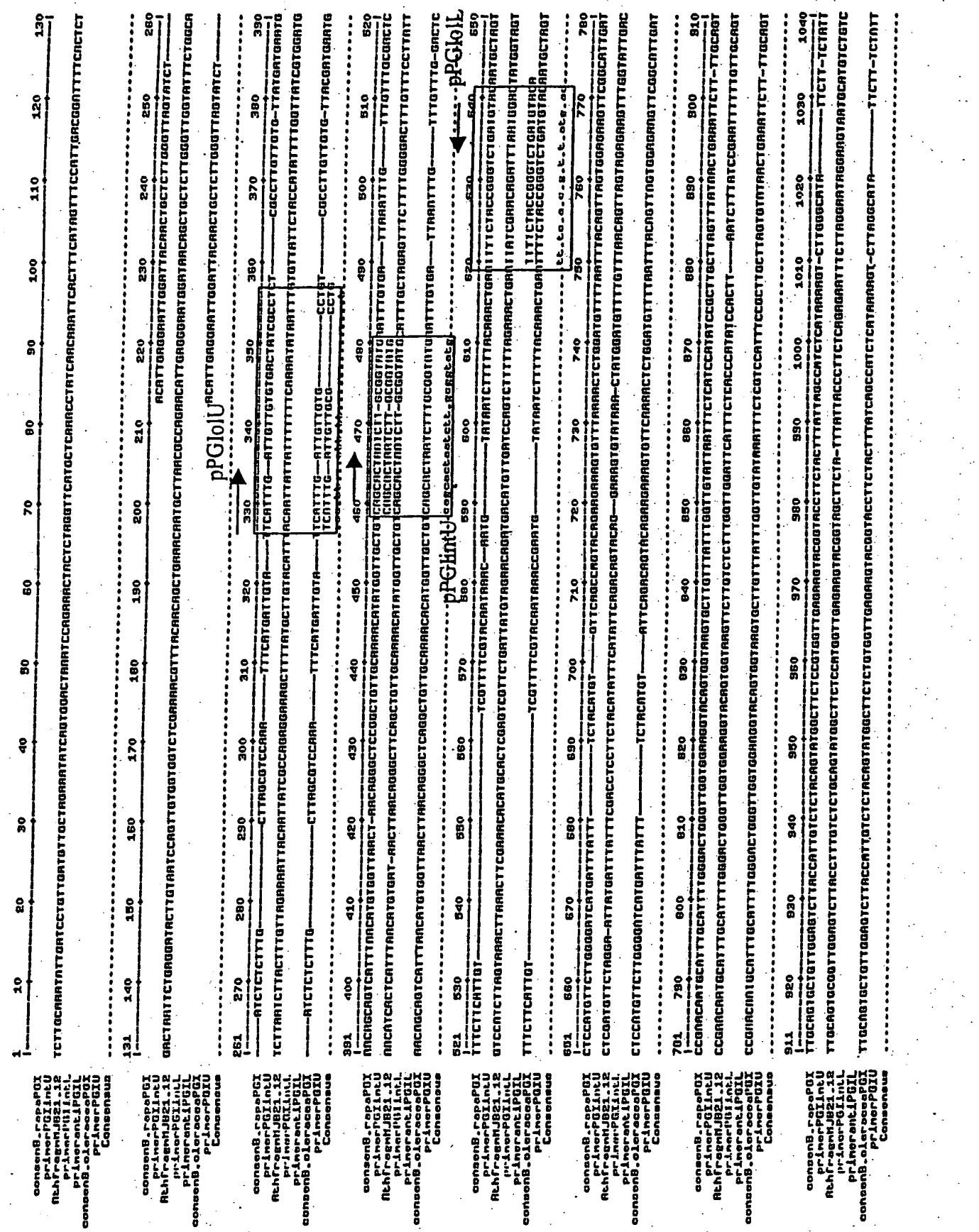


Figure 16 BIS

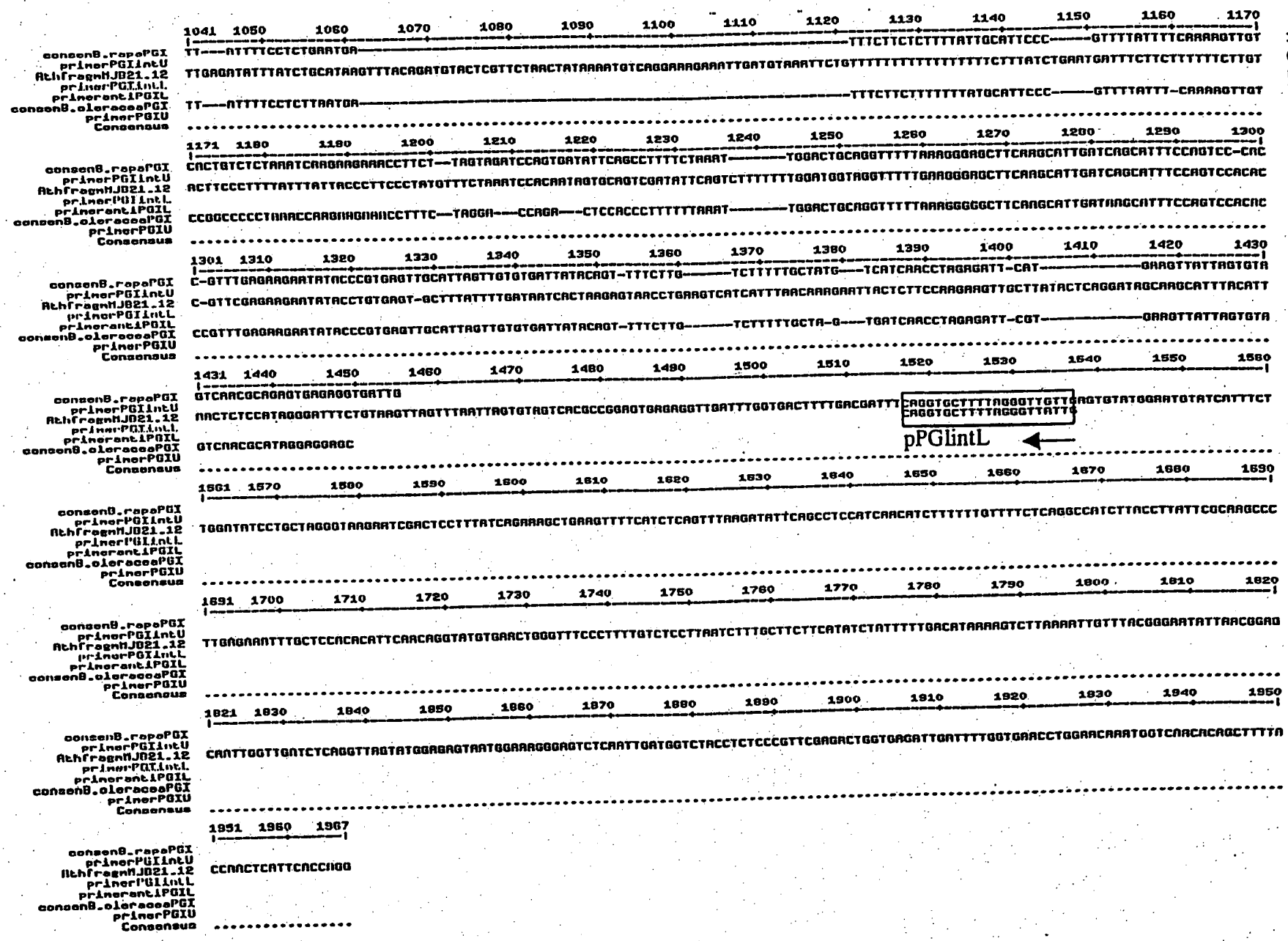
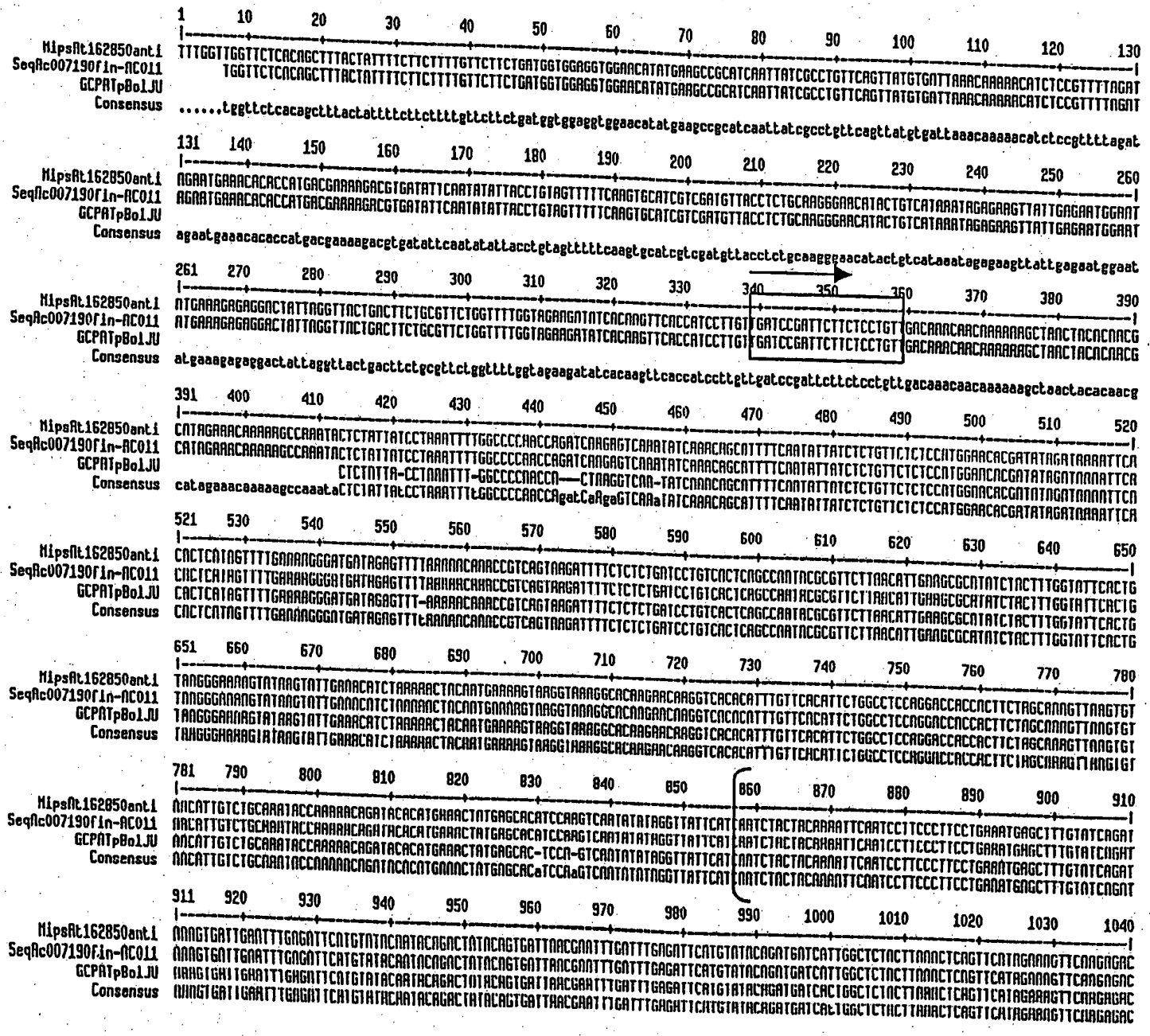


Figure 17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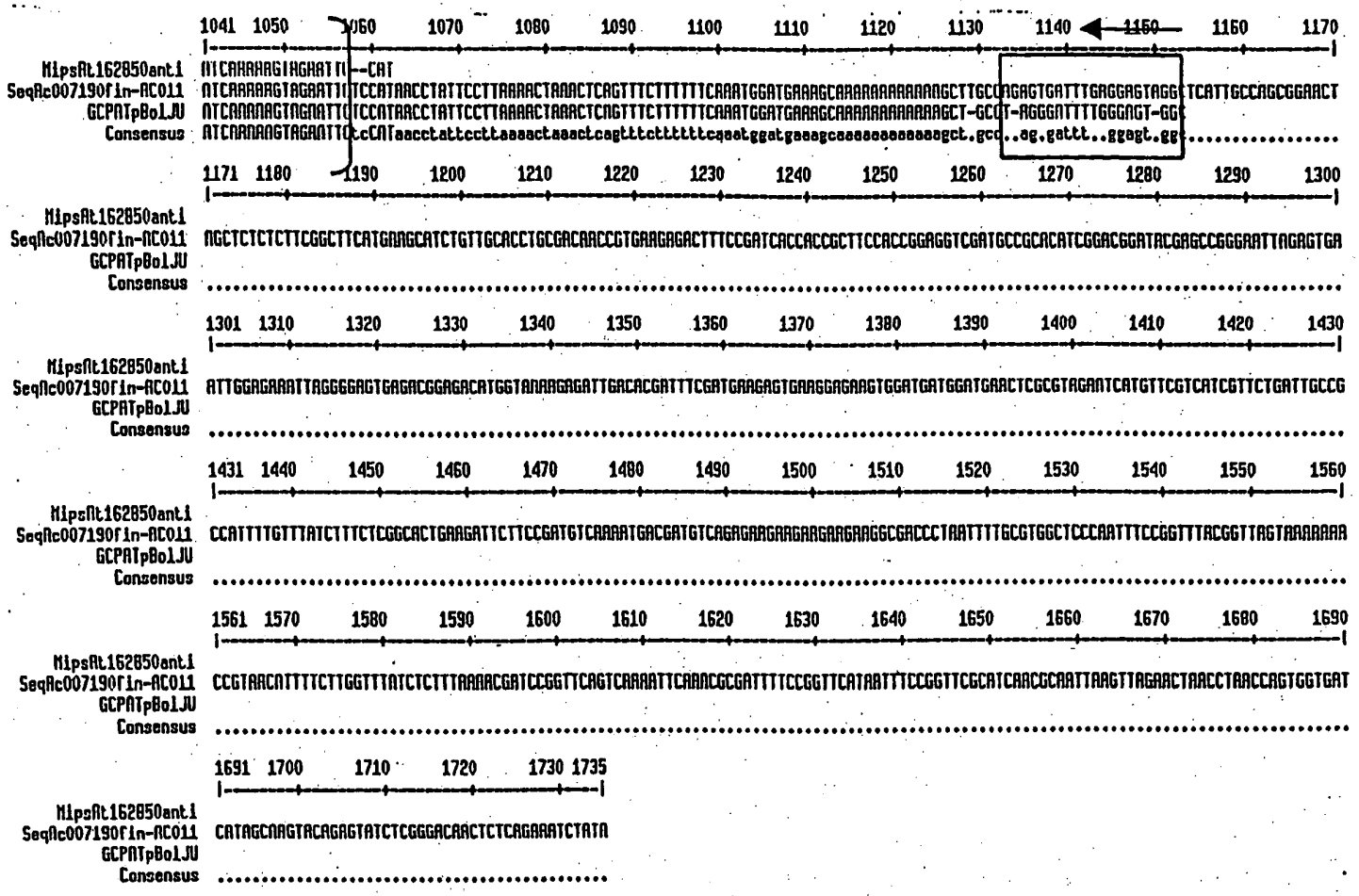
Consensus
BolJon U
about 700bp
fromAC007190
end
AC011000 start
overlapping
AC007190 end

Figure 17 BIS



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